



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/015078

Source: OIPE

Date Processed by STIC: 09/10/2001

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TECH CENTER 1600/290

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/015,078

DATE: 09/10/2001
TIME: 09:39:29

Input Set : A:\235673-1.app
Output Set: N:\CRF3\09102001\I015078.raw

*Does Not Comply
Corrected Diskette Needed*

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Suerbaum, Sebastian
7 Labigne, Agnes

9 (ii) TITLE OF INVENTION: Cloning and Characterization of the flbA
10 Gene of H. Pylori, Production of Aflagellate Strains

12 (iii) NUMBER OF SEQUENCES: 13

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
16 Dunner

17 (B) STREET: 1300 I Street, N.W.

18 (C) CITY: Washington

19 (D) STATE: D.C.

20 (E) COUNTRY: USA

21 (F) ZIP: 20005-3315

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

30 (A) APPLICATION NUMBER: US/09/015,078

C--> 31 (B) FILING DATE: 23-Aug-2001

32 (C) CLASSIFICATION:

34 (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Meyers, Kenneth J.

36 (B) REGISTRATION NUMBER: 25,146

37 (C) REFERENCE/DOCKET NUMBER: 02356.0073-01000

39 (ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: (202) 408-4000

41 (B) TELEFAX: (202) 408-4400

44 (2) INFORMATION FOR SEQ ID NO: 1:

46 (i) SEQUENCE CHARACTERISTICS:

47 (A) LENGTH: 19 base pairs

48 (B) TYPE: nucleic acid

49 (C) STRANDEDNESS: single

50 (D) TOPOLOGY: linear

52 (ii) MOLECULE TYPE: DNA (genomic)

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

59 ATGCCNGGNA AAGCARATG

19

61 (2) INFORMATION FOR SEQ ID NO: 2:

63 (i) SEQUENCE CHARACTERISTICS:

64 (A) LENGTH: 18 base pairs

65 (B) TYPE: nucleic acid

66 (C) STRANDEDNESS: single

67 (D) TOPOLOGY: linear

69 (ii) MOLECULE TYPE: DNA (genomic)

Errored: Sequence listing must conform to the rules in the CFR as of July 1, 1998.

Must use new format; Contact Robert Wex at

703 306 4119

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Input Set : A:\235673-1.app
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74	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
76	RAAYTTCATN GCNCRTC	18
78	(2) INFORMATION FOR SEQ ID NO: 3:	
80	(i) SEQUENCE CHARACTERISTICS:	
81	(A) LENGTH: 135 base pairs	
82	(B) TYPE: nucleic acid	
83	(C) STRANDEDNESS: single	
84	(D) TOPOLOGY: linear	
86	(ii) MOLECULE TYPE: DNA (genomic)	
91	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:	
93	ATGCCAGGAA AGCAAATGGC GATTGATGCG GATTAAATT CAGGGCTTAT TGATGATAAG	60
95	GAAGCTAAAA AACGGCGCGC CGCTCTAACGC CAAGAAGCGG ATTTTTATGG TGCGATGGAT	120
97	GGCGCGTCTA AATT	135
99	(2) INFORMATION FOR SEQ ID NO: 4:	
101	(i) SEQUENCE CHARACTERISTICS:	
102	(A) LENGTH: 28 base pairs	
103	(B) TYPE: nucleic acid	
104	(C) STRANDEDNESS: single	
105	(D) TOPOLOGY: linear	
107	(ii) MOLECULE TYPE: DNA (genomic)	
112	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:	
114	CGGGATCCGT GGTTACTAAT GGTTCTAC	28
116	(2) INFORMATION FOR SEQ ID NO: 5:	
118	(i) SEQUENCE CHARACTERISTICS:	
119	(A) LENGTH: 28 base pairs	
120	(B) TYPE: nucleic acid	
121	(C) STRANDEDNESS: single	
122	(D) TOPOLOGY: linear	
124	(ii) MOLECULE TYPE: DNA (genomic)	
129	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
131	CGGGATCCCTC ATGGCCTCTT CAGAGACC	28
133	(2) INFORMATION FOR SEQ ID NO: 6:	
135	(i) SEQUENCE CHARACTERISTICS:	
136	(A) LENGTH: 2501 base pairs	
137	(B) TYPE: nucleic acid	
138	(C) STRANDEDNESS: single	
139	(D) TOPOLOGY: linear	
141	(ii) MOLECULE TYPE: DNA (genomic)	
146	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:	
148	AGCTTTTTTG TGCCATACTT TTAAACTTA TATTATAATA AGAGACAAAC ACACCTACCA	60
150	AAATTAAGGC ATTGATTAA GATTATGGCA AACGAACGCT CCAAATTAGC TTTTAAAAAG	120
152	ACTTTCCCTG TCTTAAACG CTTCTTGCAA TCCAAAGACT TAGCCCTTGT GGTCTTTGTG	180
154	ATAGCGATT TAGCGATCAT TATCGTGCGC TTACCGCCTT TTGTGTTGGA TTTTTTACTC	240
156	ACGATTTCATA TCGCGCTATC GGTGTTGATT ATTTTAATCG GGCTTTATAT TGACAAACCG	300
158	ACTGATTTTA GCGCTTCCC CACTTTATTA CTCATTGAA CCTTATAACCG CTTGGCTTTA	360
160	AATGTCGCCA CCACTAGAAT GATTTTAACC CAAGGCTATA AAGGGCCTAG CGCGGTGAGC	420
162	ATTATTATCA CGGCGTTGG GGAATTTCAGC GTGAGCGGGGA ATTATGTGAT TGGGGCTATT	480
164	ATCTTTAGTA TTTTAGTGCT GGTGAATTAA TTAGTGGTTA CTAATGGTC TACTAGGGTT	540
166	ACTGAAGTTA GGGCGCGATT TGCCCTAGAC GCTATGCCAG GAAAGCAAAT GGCGATTGAT	600

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168	CGGGATTAA	ATTCAGGGCT	TATTGATGAT	AAGGAAGCTA	AAAAACGGCG	CGCCGCTCTA	660
170	AGCCAAGAAG	CGGATTTTA	TGGTGCATG	GATGGCGCGT	CTAAATTGT	CAAAGGCGAT	720
172	GCGATCGCTT	CTATCATTAT	CACGCTTATC	AATATCATTG	GGGGTTTTT	AGTGGCGTG	780
174	TTCCAAAGGG	ATATGAGCTT	GAGCTTAGT	GCTAGCACTT	TCACTATCTT	AACCATTGGC	840
176	GATGGGCTTG	TAGGGCAAAT	CCCTGCCTTA	ATCATTGCAG	CACGGACCAG	TATTGTCGCC	900
178	ACTCGCACCA	CGCAAAACGA	AGAAGAGGAC	TTTGCTTCTA	AGCTCATCAC	ACAGCTCAC	960
180	AATAAAAGCA	AAACTTTAGT	GATTGTGGGG	GCGATTATT	GCTTTGCAC	CATTCCCTGGA	1020
182	CTCCCTACCT	TTTCTTTAGC	GTTTGTAGGG	GCTCTCTTT	TATTCATCGC	ATGGCTGATT	1080
184	AGCAGGGAGG	GAAAGGACGG	GTTGCTCACT	AAATTAGAAA	ATTATTTGAG	TCAAAATTC	1140
186	GGCTTGGATT	TGAGCGAAA	ACCCCACAGC	TCCAAAATCA	AACCCACGC	CCCCACCACA	1200
188	AGGGCTAAAA	CCCAAGAAGA	GATTAAAAGA	GAAGAAGAGC	AAGCCATTGA	TGAAGTGT	1260
190	AAAATTGAAT	TTTTAGAATT	GGCTTTAGGC	TATCAGCTCT	ACAGCTTAGC	GGACATGAAA	1320
192	CAAGGGGCG	ATTGTTAGA	AAGGATTAGG	GGTATTAGAA	AAAAGATAGC	GAGCGATTAT	1380
194	GGTTTTTGA	TGCCTCAAAT	TAGGATTAGG	GATAATTTAC	AACTCCCCC	AACGCATTAT	1440
196	GAAATCAAGC	TTAAGGGCAT	TGTGATTGGT	GAAGGCATGG	TGATGCCGGA	TAAGTTTTA	1500
198	GCCATGAATA	CCGGTTTGT	GAATAAAAGAA	ATTGAAGGCA	TTCCTACTAA	AGAGCCGGCT	1560
200	TTTGGAAATGG	ACGCTTTATG	GATTGAAACT	AAAAATAAAAG	AAGAAGCCAT	CATTCAAGGC	1620
202	TATACCATTA	TTGATCCAAG	CACCGTTATT	GCGACGCACA	CCAGCGAATT	AGTAAAAAA	1680
204	TACGCTGAAG	ATTTTATCAC	TAAAGATGAA	GTGAAATCCC	TTTTAGAGCG	CTTGGCCAAA	1740
206	GACTATCCTA	CGATTGTAGA	AGAGAGTAA	AAAATCCCCA	CCGGTGCAG	CCGATCAGTC	1800
208	TTGCAAGCCT	TGTTGCATGA	AAAAATCCCC	ATTAAGACAA	TGCTCACTAT	TTTAGAAACG	1860
210	ATTACCGATA	TTGCGCCATT	AGTCAAAAC	GATGTGAATA	TCTTAACCGA	ACAAGTGAGG	1920
212	GCGAGGCTTT	CTAGGGTGAT	CACTAACGCT	TTAAATCTG	AAGACGGCG	TTGAAATT	1980
214	TTAACCTTT	CTACCGATAG	CGAACAAATT	TTGCTTAATA	AATTGCGAGA	AAATGGCACT	2040
216	TCTAAGAGCC	TACTACTCAA	TGTGGGCCAA	TTGCAAAAC	TCATTGAAGC	GGTCTCTGAA	2100
218	GAGGCCATGA	AAGTCTTGCA	AAAAGGGATC	GCTCCGGTGA	TTTGATCGT	AGAGCCTAAT	2160
220	TTAAGAAAAG	CCCTTTCTAA	TCAAATGGAG	CAGGCTAGGA	TTGATGTAAT	CGTCTAAC	2220
222	CATGCTGAAT	TAGATCCTAA	CTCTAATT	GAAGCCTTAG	GCACGATCCA	TATTAACTTT	2280
224	TAAGGGATAA	ATAATTGATA	AAAAGGAGA	ATGATGCAAG	TTTATCACCT	TTCACACATT	2340
226	GATTTAGACG	GCTATGCATG	CCAGCTTGT	TCAAAACAAT	TTTTAAAAAA	TATCCAATGC	2400
228	TATAACGCTA	ATTACGGGCG	TGAAGTCTCA	GCGAGAATT	ATGAGATT	AAACCGCATC	2460
230	GCTCAATCTA	AAGAGAGTGA	ATTCTTATT	TTGATTAGCG	A		2501

232 (2) INFORMATION FOR SEQ ID NO: 7:

234 (i) SEQUENCE CHARACTERISTICS:

235 (A) LENGTH: 732 amino acids

236 (B) TYPE: amino acid

237 (C) STRANDEDNESS: single

238 (D) TOPOLOGY: linear

240 (ii) MOLECULE TYPE: peptide

245 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

247	Met	Ala	Asn	Glu	Arg	Ser	Lys	Leu	Ala	Phe	Lys	Lys	Thr	Phe	Pro	Val
248	1				5				10				15			
250	Phe	Lys	Arg	Phe	Leu	Gln	Ser	Lys	Asp	Leu	Ala	Leu	Val	Val	Phe	Val
251					20				25				30			
253	Ile	Ala	Ile	Leu	Ala	Ile	Ile	Ile	Val	Pro	Leu	Pro	Pro	Phe	Val	Leu
254					35				40				45			
256	Asp	Phe	Leu	Leu	Thr	Ile	Ser	Ile	Ala	Leu	Ser	Val	Leu	Ile	Ile	Leu
257					50				55				60			
259	Ile	Gly	Leu	Tyr	Ile	Asp	Lys	Pro	Thr	Asp	Phe	Ser	Ala	Phe	Pro	Thr

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260	65	70	75	80												
262	Leu	Leu	Leu	Ile	Val	Thr	Leu	Tyr	Arg	Leu	Ala	Leu	Asn	Val	Ala	Thr
263																
265		85							90							95
266	Thr	Arg	Met	Ile	Leu	Thr	Gln	Gly	Tyr	Lys	Gly	Pro	Ser	Ala	Val	Ser
268																
269		100							105							110
271	Ile	Ile	Ile	Thr	Ala	Phe	Gly	Glu	Phe	Ser	Val	Ser	Gly	Asn	Tyr	Val
272																
274		115							120							125
275	Ile	Gly	Ala	Ile	Ile	Phe	Ser	Ile	Leu	Val	Leu	Val	Asn	Leu	Leu	Val
277																
278		130							135							140
280	Val	Thr	Asn	Gly	Ser	Thr	Arg	Val	Thr	Glu	Val	Arg	Ala	Arg	Phe	Ala
281																
283	145		150							155						160
284	Leu	Asp	Ala	Met	Pro	Gly	Lys	Gln	Met	Ala	Ile	Asp	Ala	Asp	Leu	Asn
286																
288	165									170						175
289	Ser	Gly	Leu	Ile	Asp	Asp	Lys	Glu	Ala	Lys	Lys	Arg	Arg	Ala	Ala	Leu
290																
292	180								185							190
293	Ser	Gln	Glu	Ala	Asp	Phe	Tyr	Gly	Ala	Met	Asp	Gly	Ala	Ser	Lys	Phe
294																
295	195								200							205
296	Val	Lys	Gly	Asp	Ala	Ile	Ala	Ser	Ile	Ile	Ile	Thr	Leu	Ile	Asn	Ile
297										215						220
298	210															
299	Ile	Gly	Gly	Phe	Leu	Val	Gly	Val	Phe	Gln	Arg	Asp	Met	Ser	Leu	Ser
300																
301	225		230							235						240
302	Phe	Ser	Ala	Ser	Thr	Phe	Thr	Ile	Leu	Thr	Ile	Gly	Ala	Gly	Leu	Val
303																
304	245									250						255
305	Gly	Gln	Ile	Pro	Ala	Leu	Ile	Ile	Ala	Thr	Arg	Thr	Gly	Ile	Val	Ala
306																
307	260								265							270
308	Thr	Arg	Thr	Thr	Gln	Asn	Glu	Glu	Glu	Asp	Phe	Ala	Ser	Lys	Leu	Ile
309																
310	275								280							285
311	Thr	Gln	Leu	Thr	Asn	Lys	Ser	Lys	Thr	Leu	Val	Ile	Val	Gly	Ala	Ile
312										295						300
313	290															
314	Tyr	Cys	Phe	Cys	Thr	Ile	Pro	Gly	Leu	Pro	Thr	Phe	Ser	Leu	Ala	Phe
315									310							320
316	305									315						
317	Val	Gly	Ala	Leu	Phe	Leu	Phe	Ile	Ala	Trp	Leu	Ile	Ser	Arg	Glu	Gly
318																
319	325									330						335
320	Lys	Asp	Gly	Leu	Leu	Thr	Lys	Leu	Glu	Asn	Tyr	Leu	Ser	Gln	Lys	Phe
321										340						350
322	340									345						
323	Gly	Leu	Asp	Leu	Ser	Glu	Lys	Pro	His	Ser	Ser	Lys	Ile	Lys	Pro	His
324										355						365
325	350									360						
326	Ala	Pro	Thr	Thr	Arg	Ala	Lys	Thr	Gln	Glu	Glu	Ile	Lys	Arg	Glu	Glu
327										370						380
328	Glu	Gln	Ala	Ile	Asp	Glu	Val	Leu	Lys	Ile	Glu	Phe	Leu	Glu	Leu	Ala
329										385						400
330	Leu	Gly	Thr	Gln	Leu	Tyr	Ser	Leu	Ala	Asp	Met	Lys	Gln	Gly	Gly	Asp
331										390						415
332	405									410						
333	Leu	Leu	Glu	Arg	Ile	Arg	Gly	Ile	Arg	Lys	Lys	Ile	Ala	Ser	Asp	Tyr
334										420						430
335	Gly	Phe	Leu	Met	Pro	Gln	Ile	Arg	Ile	Arg	Asp	Asn	Leu	Gln	Leu	Pro
336										435						445
337	450									440						
338	Pro	Thr	His	Tyr	Glu	Ile	Lys	Leu	Lys	Gly	Ile	Val	Ile	Gly	Glu	Gly
339										455						460

RAW SEQUENCE LISTING
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Input Set : A:\235673-1.app
Output Set: N:\CRF3\09102001\I015078.raw

334 Met Val Met Pro Asp Lys Phe Leu Ala Met Asn Thr Gly Phe Val Asn
335 465 470 475 480
337 Lys Glu Ile Glu Gly Ile Pro Thr Lys Glu Pro Ala Phe Gly Met Asp
338 485 490 495
340 Ala Leu Trp Ile Glu Thr Lys Asn Lys Glu Glu Ala Ile Ile Gln Gly
341 500 505 510
343 Tyr Thr Ile Ile Asp Pro Ser Thr Val Ile Ala Thr His Thr Ser Glu
344 515 520 525
346 Leu Val Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val Lys
347 530 535 540
349 Ser Leu Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu Glu
350 545 550 555 560
352 Ser Lys Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala Leu
353 565 570 575
355 Leu His Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu Thr
356 580 585 590
358 Ile Thr Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu Thr
359 595 600 605
361 Glu Gln Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe Lys
362 610 615 620
364 Ser Glu Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Ser Glu
365 625 630 635 640
367 Gln Phe Leu Leu Asn Lys Leu Arg Glu Asn Gly Thr Ser Lys Ser Leu
368 645 650 655
370 Leu Leu Asn Val Gly Glu Leu Gln Lys Leu Ile Glu Ala Val Ser Glu
371 660 665 670
373 Glu Ala Met Lys Val Leu Gln Lys Gly Ile Ala Pro Val Ile Leu Ile
374 675 680 685
376 Val Glu Pro Asn Leu Arg Lys Ala Leu Ser Asn Gln Met Glu Gln Ala
377 690 695 700
379 Arg Ile Asp Val Ile Val Leu Ser His Ala Glu Leu Asp Pro Asn Ser
380 705 710 715 720
382 Asn Phe Glu Ala Leu Gly Thr Ile His Ile Asn Phe
383 725 730
385 (2) INFORMATION FOR SEQ ID NO: 8:
387 (i) SEQUENCE CHARACTERISTICS:
388 (A) LENGTH: 732 amino acids
389 (B) TYPE: amino acid
390 (C) STRANDEDNESS: single
391 (D) TOPOLOGY: linear
393 (ii) MOLECULE TYPE: peptide
398 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
400 Met Ala Asn Glu Arg Ser Lys Leu Ala Phe Lys Lys Thr Phe Pro Val
401 1 5 10 15
403 Phe Lys Arg Phe Leu Gln Ser Lys Asp Leu Ala Leu Val Val Phe Val
404 20 25 30
406 Ile Ala Ile Leu Ala Ile Ile Ile Val Pro Leu Pro Pro Phe Val Leu
407 35 40 45
409 Asp Phe Leu Leu Thr Ile Ser Ile Ala Leu Ser Val Leu Ile Ile Leu

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/015,078

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Input Set : A:\235673-1.app

Output Set: N:\CRF3\09102001\I015078.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]